

Figure 1.
Typical electropherograms for the AGC 1 locus; all samples are from within West Virginia.

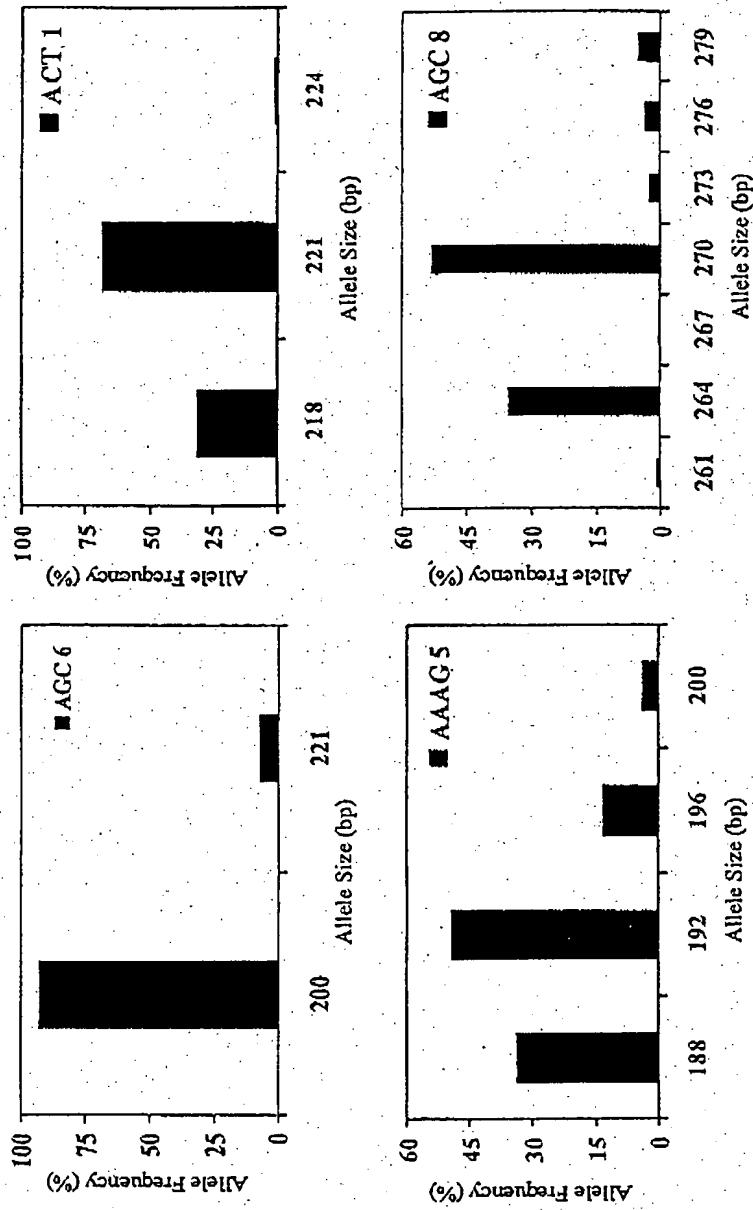


Figure 2.
Allele frequency distributions for all eight loci, across all 295 samples that were genotyped

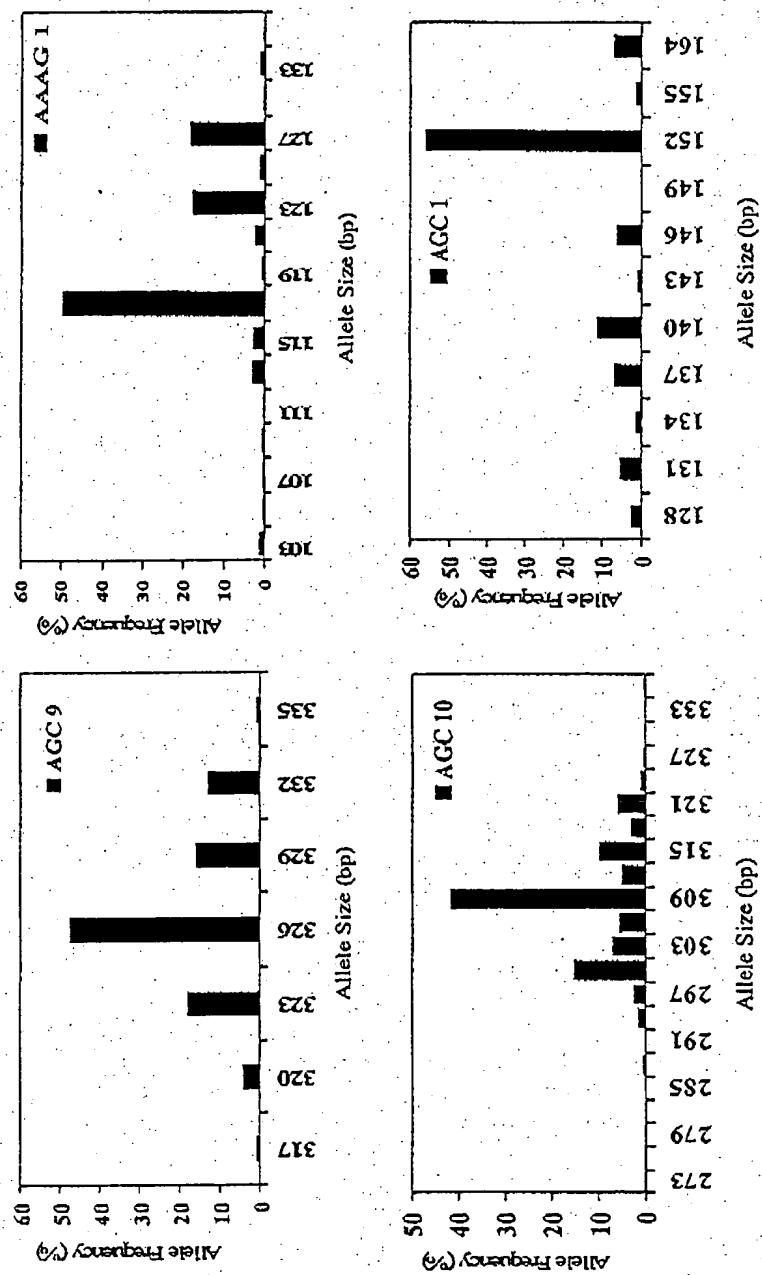


Figure 2 continued...

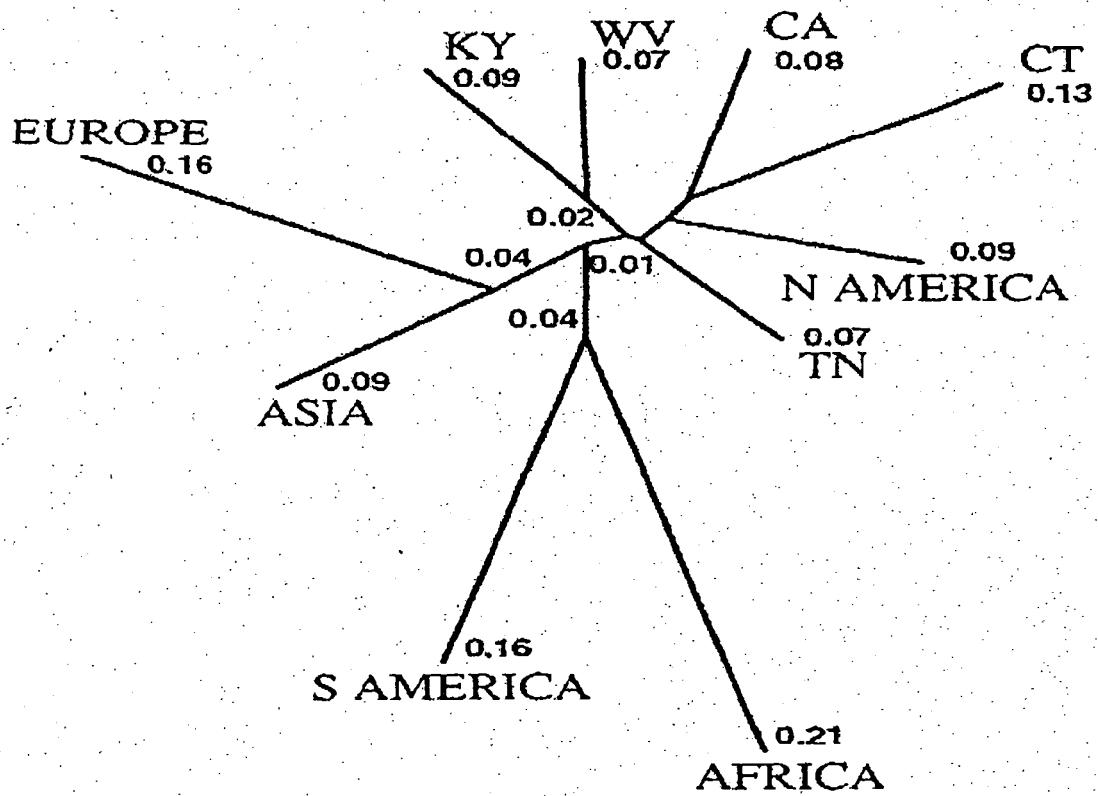
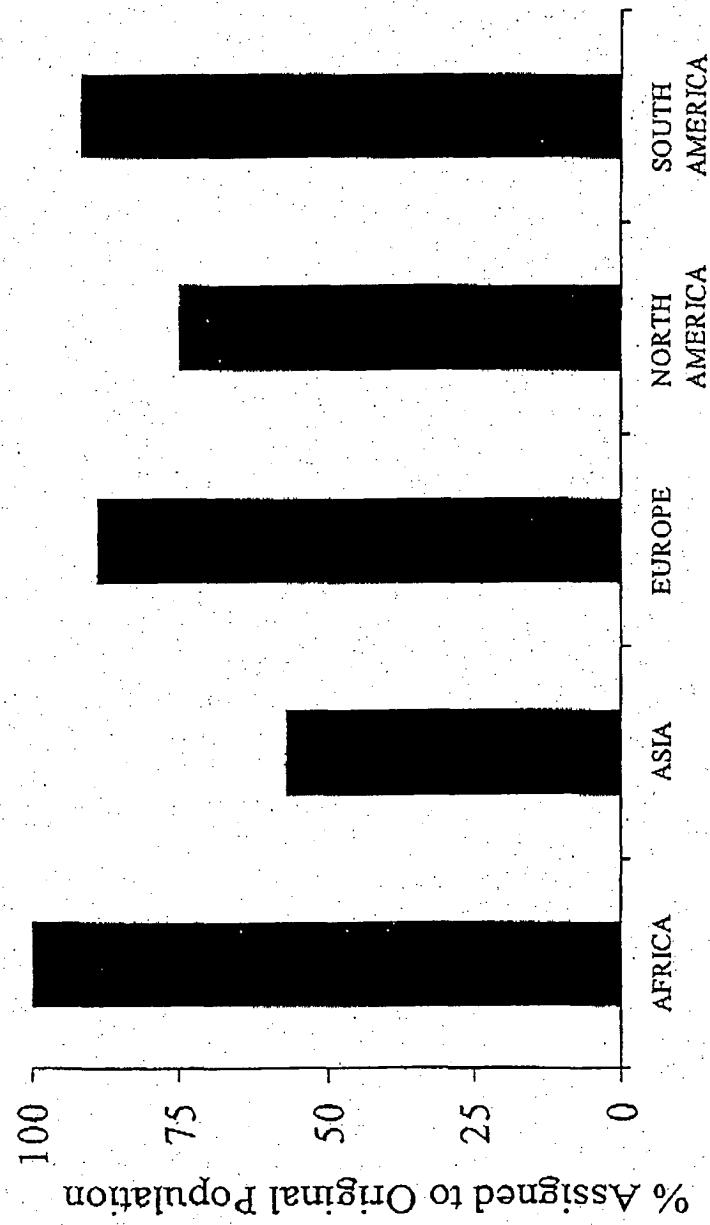


Figure 3.
 Neighbor-joining tree constructed with the genotypic profiles of 295 *Cannabis sativa* samples. The distance matrix used to construct this tree was calculated as a comparison of the proportion of shared alleles.



Original Cannabis Population

Figure 4.
The assignment test results from all 295 samples reveal that at least 50% of the time a genotypic profile can correctly be assigned to the original population from which the sample came from.

Source of variation	d.f.	Sum of squares	Variance components	Percentage of variation
Among Continents	2	54.559	0.05441 Va	2.24
Among Countries within Continents	2	26.508	0.18956 Vb	7.81
Within Countries And States	585	1276.328	2.18176 Vc	89.94
Total	589	1357.395	2.42573	
Fixation Indices				
FST:	0.10058			
FSC:	0.07994			
FCT:	0.02243			

Figure 5.

Analysis of Molecular Variance (AMOVA) demonstrates that the greatest proportion (~ 90%) of genetic variation in this system lies within countries and states, at the individual sample level. Statistically significant values ($P < 0.00001$)